



SUBSTITUTE SEQUENCE LISTING

<110> Sleeman, Matthew
Murison, Greg

<120> Fibroblast Growth Factor Receptors and Methods for Their Use

<130> 11000.1037c5

<150> U.S. 09/823,038

<151> 2001-03-28

<150> U.S. 09/383,586

<151> 1999-08-26

<150> U.S. 09/276,268

<151> 1999-03-25

<150> PCT/NZ00/00015

<151> 2000-02-18

<150> U.S. 60/221,216

<151> 2000-07-25

<150> U.S. 10/157,444

<151> 2000-05-28

<150> PCT/NZ03/00105

<151> 2003-05-27

<160> 145

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ctgcctaggt	gcaaatacca	tgggctacag	tttccgtagc	gccttcctca	ctgtattacc	300
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<212> DNA

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gcctggggccg	cactgtgcgg	ctacagtgcc	cagtggaggg	ggaccaccca	ccgttgacca	360
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cgcccccgcg	ctgatccctg	tcgagcgtct	acgcgcctcg	cttcctttgc	ctggagctcg	300
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gtgccagtgg	agggggaccc	gccgccgctg	accatgtgga	ccaaggatgg	ccgcaccatc		240
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Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile
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Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu
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Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser
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<211> 529

<212> PRT

<213> Mouse

<400> 6

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Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
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Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
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Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
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Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
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Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
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Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu
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 325 330 335
 Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu
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 Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser
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 Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val
 370 375 380
 Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys
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 Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile
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 Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr
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 515 520 525
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<400> 7
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 35 40 45
 Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
 50 55 60
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
 65 70 75 80
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
 85 90 95
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
 100 105 110
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
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 Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
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Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
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Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Pro	Gly	Pro	Pro	Met
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Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly
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Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys
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Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu
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<210> 8

<211> 324

<212> PRT

<213> Human

<400> 8

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Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
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Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
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Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
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Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
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caaacctcca gggcctccta tggtctcttc atcgatcatc acaagcctgc catggcctgt	960
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tggccccaag ctgtacccca agctatacac agatgtgcac acacacacac atacacacac	1260
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<400> 11
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 <212> DNA
 <213> Mouse

<400> 12
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<210> 13
 <211> 373
 <212> PRT
 <213> Mouse

<400> 13
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 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
 115 120 125
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg
 130 135 140
 Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val
 145 150 155 160
 Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro
 165 170 175
 Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala
 180 185 190
 Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys

195	200	205
Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly		
210	215	220
Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser		
225	230	235
Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe		
245	250	255
Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro		
260	265	270
Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His		
275	280	285
Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr		
290	295	300
Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu		
305	310	315
Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly		
325	330	335
Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu		
340	345	350
Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser		
355	360	365
Thr Ser Leu Pro Trp		
370		

<210> 14
 <211> 135
 <212> PRT
 <213> Mouse

<400> 14
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Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala
35 40 45
Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys
50 55 60
Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His
65 70 75 80
Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro
85 90 95
Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys
100 105 110
Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu
115 120 125
Asn Asn Gly Gly Arg Val Ser
130 135

<210> 15
 <211> 37
 <212> PRT
 <213> Mouse

<400> 15

Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val

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			20					25					30		
Pro	Asp	Gly	Ser	Tyr											
		35													

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 <211> 1515
 <212> DNA
 <213> Human

<400> 16

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ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
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<210> 17
 <211> 504
 <212> PRT
 <213> Human

<400> 17

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
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			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35				40						45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50				55						60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65				70				75						80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
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accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg    240
ccgcaggggc tgaagggtgaa gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag    300
gccaccaacg gcttcggcag ccttagcgct aactacaccc tcgtcgtgct ggatgacatt    360
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<210> 19
<211> 386
<212> PRT
<213> Human

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<400> 19
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          20          25          30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
          35          40          45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
          50          55          60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
65          70          75          80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
          85          90          95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
          100          105          110
Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
          115          120          125
Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
          130          135          140
Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile

145          150          155          160
Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly
          165          170          175
His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr

          180          185          190
Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu

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195	200	205
Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser		
210	215	220
Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile His		
225	230	235
Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser		
245	250	255
Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile		
260	265	270
Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys		
275	280	285
Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr		
290	295	300
Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu		
305	310	315
Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala		
325	330	335
Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu		
340	345	350
Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Thr His Ser		
355	360	365
His Thr His Ser His Val Glu Gly Lys Val His Gln His Ile His Tyr		
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Gln Cys		
385		

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 <211> 1230
 <212> DNA
 <213> Human

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<210> 21
 <211> 409
 <212> PRT

<213> Human

<400> 21

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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
		115					120					125			
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
	130					135					140				
Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
145					150					155					160
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
				165					170					175	
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
			180					185					190		
Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
		195					200					205			
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
	210					215					220				
Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
225					230					235					240
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
			245						250					255	
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala
			260					265					270		
Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile
		275					280					285			
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys
	290					295					300				
Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro
305					310					315					320
Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp
				325					330					335	
Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys
			340					345					350		
Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly
		355					360					365			
Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His
	370					375					380				
Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys
385					390					395					400
Val	His	Gln	His	Ile	His	Tyr	Gln	Cys							
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<211> 1434
 <212> DNA
 <213> Human

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<210> 23
 <211> 477
 <212> PRT
 <213> Human

<400> 23
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 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 115 120 125
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 130 135 140
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 145 150 155 160
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys

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ttcctcaccg	tgctgccaga	cccaaaaccg	caagggccag	ctgtggcctc	ctcgtcctcg	840
gccactagcc	tgccgtggcc	cgtgggtcatc	ggcatcccag	ccggcgctgt	cttcatcctg	900
ggcaccctgc	tcctgtgggt	ttgccaggcc	cagaagaagc	cgtgcacccc	cgcgctggcc	960
cctcccctgc	ctgggcaccg	ccgcgcgggg	acggcccgcg	accgcagcgg	agacaaggac	1020
cttccctcgt	tggcgcacct	cagcgctggc	cctgggtgtgg	ggctgtgtga	ggagcatggg	1080
tctccggcag	ccccccagca	cttactgggc	ccaggcccag	ttgctggccc	taagttgtac	1140
cccaaactct	acacagacat	ccacacacac	acacacacac	actctcacac	acactcacac	1200
gtggagggca	aggtccacca	gcacatccac	tatcagtgtc	ag		1242

<210> 25

<211> 413

<212> PRT

<213> Human

<400> 25

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
		35					40					45			
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
		50				55					60				
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
65					70					75					80
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
				85					90					95	
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
			100					105					110		
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
		115					120					125			
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
		130				135					140				
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr
145					150					155					160
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln
			165					170						175	
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg
		180						185					190		
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly
		195					200					205			
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro
		210				215					220				
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp
225					230					235					240
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser
			245						250					255	
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly
			260					265					270		
Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val
		275					280					285			
Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu
		290				295					300				
Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala
305					310					315					320

Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser
 325 330 335
 Gly Asp Lys Asp Leu Pro Ser Leu Ala Leu Ser Ala Gly Pro Gly
 340 345 350
 Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu
 355 360 365
 Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr
 370 375 380
 Thr Asp Ile His Thr His Thr His Thr His Ser His Thr His Ser His
 385 390 395 400
 Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys
 405 410

<210> 26
 <211> 876
 <212> DNA
 <213> Human

<400> 26
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 gcccggtg ggcgactgt gcggctgcag tgcccagtgg agggggaccc gccgcgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggt ggagccgctt ccgctgtctg 240
 ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacacc tcgtcgtgct ggatgacatt 360
 agcccaggga aggagagcct ggggcccagc agtcctctg ggggtcaaga ggaccccgcc 420
 agccagcagt gggacccaaa accgcaaggg ccacctgtgg cctcctcgtc ctcggccact 480
 agcctgccgt ggcccggtgt catcggcac ccagccggcg ctgtcttcat cctgggcacc 540
 ctgctcctgt ggctttgccg ggcccagaag aagccgtgca ccccgcgcc tgccctccc 600
 ctgctggggc accgcccggc ggggacggcc cgcgaccgca gcggagacaa ggacctccc 660
 tcgttgggcg cctcagcgc tggccctggt gtggggctgt gtgaggagca tgggtctccg 720
 gcagccccc agcacttact gggcccaggc ccagttgctg gccctaagtt gtacccaaa 780
 ctctacacag acatccacac acacacacac acacactctc acacacactc acacgtggag 840
 ggcaaggtcc accagcacat ccactatcag tgctag 876

<210> 27
 <211> 291
 <212> PRT
 <213> Human

<400> 27
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115 120 125

Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140
 Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser Ser Ala Thr
 145 150 155 160
 Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe
 165 170 175
 Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro
 180 185 190
 Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly
 195 200 205
 Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala
 210 215 220
 Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro
 225 230 235 240
 Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys
 245 250 255
 Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Thr His
 260 265 270
 Ser His Thr His Ser His Val Glu Gly Lys Val His Gln His Ile His
 275 280 285
 Tyr Gln Cys
 290

<210> 28

<211> 1080

<212> DNA

<213> Human

<400> 28

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgaggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgct	aactacacc	tcgtcgtgct	ggcacgaccg	360
cgcttcacac	agccctccaa	gatgaggcgc	cgggtgatcg	cacggcccgt	gggtagctcc	420
gtgcggctca	agtgcgtggc	cagcgggcac	cctcggcccc	acatcacgtg	gatgaaggac	480
gaccaggcct	tgacgcgccc	agaggccgct	gagcccagga	agaagaagtg	gacactgagc	540
ctgaagaacc	tgcggccgga	ggacagcggc	aaatacacct	gccgcgtgtc	gaaccgcgcg	600
ggcgccatca	acgccaccta	caaggtggat	gtgatccacc	caaaaccgca	agggccacct	660
gtggcctcct	cgtcctcggc	cactagcctg	ccgtggcccc	tggtcatcgg	catcccagcc	720
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tgcacccccg	cgcttgcccc	tcccctgcct	gggcaccgcc	cgccggggac	ggcccgcgac	840
cgcagcggag	acaaggacct	tccctcgttg	gccgccctca	gcgctggccc	tggtgtgggg	900
ctgtgtgagg	agcatgggtc	tccggcagcc	ccccagcact	tactggggcc	aggcccagtt	960
gctggcccta	agttgtaccc	caaactctac	acagacatcc	acacacacac	acacacacac	1020
tctcacacac	actcacacgt	ggagggcaag	gtccaccagc	acatccacta	tcagtgtctag	1080

<210> 29

<211> 359

<212> PRT

<213> Human

<400> 29

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala

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cgctgggagt	acggcgccga	gggcccgcac	aactccacca	tcgatgtggg	cggccagaag	540
tttgtggtgc	tgcccacggg	tgacgtgtgg	tcgcggcccg	acggctccta	cctcaataag	600
ctgctcatca	cccgtgcccg	ccaggacgat	gcgggcatgt	acatctgcct	tggcgccaac	660
accatggggt	acagcttccg	cagcgccttc	ctcaccgtgc	tgccagaccc	aaaaccgcaa	720
ggggccacctg	tggcctcctc	gtcctcggcc	actagcctgc	cgtggcccg	ggatcatcggc	780
atcccagccg	gcgctgtctt	catcctgggc	accctgctcc	tgtggctttg	ccaggcccag	840
aagaagccgt	gcacccccgc	gcctgcccct	cccctgcctg	ggcaccgccc	gccggggacg	900
gcccgcgacc	gcagcggaga	caaggacctt	ccctcgttgg	ccgccctcag	cgctggccct	960
ggtgtggggc	tgtgtgagga	gcatgggtct	ccggcagccc	cccagcactt	actggggcca	1020
ggcccagttg	ctggccctaa	gttgtacccc	aaactctaca	cagacatcca	cacacacaca	1080
cacacacact	ctcacacaca	ctcacacgtg	gagggcaagg	tccaccagca	catccactat	1140
cagtgcctag						1149

<210> 31
 <211> 382
 <212> PRT
 <213> Human

<400> 31

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met
			20					25					30	Ala
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val
			35				40					45		Arg
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp
			50				55				60			Thr
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val
65					70				75					80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly
				85					90					95
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn
			100					105					110	Tyr
Thr	Leu	Val	Val	Leu	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr
			115				120					125		Gly
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser
	130					135					140			Phe
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu
145					150				155					160
Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp
				165					170				175	Val
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser
			180					185					190	Arg
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg
			195				200					205		Gln
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly
	210					215					220			Tyr
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro
225					230				235					Gln
Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp
				245					250				255	Pro
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr
			260				265					270		Leu
Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala
		275					280					285		Pro

Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
130						135					140				
Val	Asp	Val	Ile	His	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser
145					150					155					160
Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala
				165					170					175	
Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala
			180					185					190		
Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His
		195					200					205			
Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro
	210					215					220				
Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu
225					230					235					240
His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val
				245					250					255	
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His
			260					265					270		
Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His
		275					280					285			
Gln	His	Ile	His	Tyr	Gln	Cys									
	290					295									

<210> 34

<211> 957

<212> DNA

<213> Human

<400> 34

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tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	agcggaccgc	ttccaagccc	180
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cagtgaagg	tgcgagcga	cgtgaagccg	gtgatccagt	ggctgaagcg	cgtggagtac	300
ggcgccgagg	gccgccacaa	ctccaccatc	gatgtgggcg	gccagaagtt	tgtggtgctg	360
cccacgggtg	acgtgtggtc	gcggccccgc	ggctcctacc	tcaataagct	gctcatcacc	420
cgtgcccgcc	aggacgatgc	gggcatgtac	atctgccttg	gcgccaacac	catgggctac	480
agcttccgca	gcgccttcct	caccgtgctg	ccagacccaa	aaccgcaagg	gccacctgtg	540
gcctcctcgt	cctcggccac	tagcctgccg	tggcccgtgg	tcacggcat	cccagccggc	600
gctgtcttca	tcctgggcac	cctgctcctg	tggctttgcc	aggcccagaa	gaagccgtgc	660
acccccgcgc	ctgcccctcc	cctgcttggg	caccgcccgc	cggggacggc	ccgcgaccgc	720
agcggagaca	aggaccttcc	ctcgttggcc	gccctcagcg	ctggccctgg	tgtggggctg	780
tgtgaggagc	atgggtctcc	ggcagccccc	cagcacttac	tgggcccagg	cccagttgct	840
ggccctaagt	tgtaccccaa	actctacaca	gacatccaca	cacacacaca	cacacactct	900
cacacacact	cacacgtgga	gggcaaggtc	caccagcaca	tccactatca	gtgctag	957

<210> 35

<211> 318

<212> PRT

<213> Human

<400> 35

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro

35	40	45
Ala Ser Gln Gln Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly		
50	55	60
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe		
65	70	75
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys		
85	90	95
Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val		
100	105	110
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg		
115	120	125
Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln		
130	135	140
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr		
145	150	155
Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Gln		
165	170	175
Gly Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro		
180	185	190
Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu		
195	200	205
Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro		
210	215	220
Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg		
225	230	235
Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro		
245	250	255
Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His		
260	265	270
Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu		
275	280	285
Tyr Thr Asp Ile His Thr His Thr His Thr His Ser His Thr His Ser		
290	295	300
His Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys		
305	310	315

<210> 36
 <211> 1161
 <212> DNA
 <213> Human

<400> 36

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gtgatcgcac	ggcccgtggg	tagctccgtg	cggtcgaagt	gcgtggccag	cgggcaccct	180
cggcccgaca	tcacgtggat	gaaggacgac	caggccttga	cgcgcccaga	ggccgctgag	240
cccaggaaga	agaagtggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacctgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacg	ccacctacaa	ggtggatgtg	360
atccagcgga	cccgttccaa	gcccgtgctc	acaggcacgc	accccgtaga	cacgacggtg	420
gacttcgggg	ggaccacgtc	cttccagtgc	aaggtgcgca	gcgacgtgaa	gccggtgatc	480
cagtggctga	agcgcgtgga	gtacggcgcc	gagggccgcc	acaactccac	catcgatgtg	540
ggcggccaga	agtttggtgt	gctgcccacg	ggtgacgtgt	ggtcgcggcc	cgacggctcc	600
tacctcaata	agctgctcat	cacccgtagc	cgccaggacg	atgcgggcat	gtacatctgc	660
cttggcgcca	acaccatggg	ctacagcttc	cgcagcgcct	tcctcaccgt	gctgccagac	720
ccaaaaccgc	aagggccacc	tgtggcctcc	tcgtcctcgg	ccactagcct	gccgtggccc	780
gtggtcatcg	gcatcccagc	cggcgctgtc	ttcatcctgg	gcaccctgct	cctgtggctt	840
tgccaggccc	agaagaagcc	gtgcaccccc	gcgcctgccc	ctccctgccc	tgggcaccgc	900

ccgccgggga	cggcccgcca	ccgcagcgga	gacaaggacc	ttccctcggt	ggccgcctc	960
agcgctggcc	ctggtgtggg	gctgtgtgag	gagcatgggt	ctccggcagc	ccccagcac	1020
ttactgggccc	caggcccagt	tgctggccct	aagttgtacc	ccaaactcta	cacagacatc	1080
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cacatccact	atcagtgcta	g				1161

<210> 37
 <211> 386
 <212> PRT
 <213> Human

<400> 37

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr
			20					25				30			
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser
		35					40					45			
Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile
	50					55					60				
Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu
65				70						75					80
Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu
			85						90					95	
Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile
			100					105					110		
Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro
		115					120					125			
Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly
	130					135					140				
Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile
145				150						155					160
Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser
			165						170					175	
Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp
		180						185					190		
Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr
	195						200					205			
Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn
	210					215					220				
Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp
225				230						235					240
Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser
			245						250					255	
Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile
		260						265					270		
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys
	275						280					285			
Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr
	290					295					300				
Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu
305				310					315						320
Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala
			325						330					335	
Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu
		340						345					350		
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser

Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu
195 200 205
Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro
210 215 220
Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
225 230 235 240
His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val
245 250 255
His Gln His Ile His Tyr Gln Cys
260

<210> 40
<211> 603
<212> DNA
<213> Human

<400> 40
atgacgccga gccccctggt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
ccggccgccg ccgcccagaga tgacattagc ccagggaagg agagcctggg gcccagacagc 120
tcctctgggg gtcaagagga ccccgccagc cagcagtggg acccaaaacc gcaagggcca 180
cctgtggcct cctcgtcctc ggccactagc ctgccgtggc ccgtgggtcat cggcatccca 240
gccggcgctg tcttcatect gggcacctg ctctctgtggc ttgcccaggc ccagaagaag 300
ccgtgcaccc ccgcgcctgc cctccccctg cctgggcacc gcccgccggg gacggcccgc 360
gaccgcagcg gagacaagga ccttcctcgt ttggccgccc tcagcgctgg ccctgggtgtg 420
gggctgtgtg aggagcatgg gtctccggca gccccccagc acttactggg cccaggccca 480
gttgctggcc ctaagtgtga ccccaaaactc tacacagaca tccacacaca cacacacaca 540
cactctcaca cacactcaca cgtggagggc aaggtccacc agcacatcca ctatcagtgc 600
tag 603

<210> 41
<211> 200
<212> PRT
<213> Human

<400> 41
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
20 25 30
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
35 40 45
Ala Ser Gln Gln Trp Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser
50 55 60
Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro
65 70 75 80
Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln
85 90 95
Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly
100 105 110
His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu
115 120 125
Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu
130 135 140
Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro
145 150 155 160
Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
165 170 175

His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val
180 185 190
His Gln His Ile His Tyr Gln Cys
195 200

<210> 42
<211> 807
<212> DNA
<213> Human

<400> 42
atgacgccga gccccctggt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
ccggccgcgc ccgcccagag acgaccgcgc ttcacacagc cctccaagat gaggcgccgg 120
gtgatcgcac ggcccgtggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180
cggcccagaca tcacgtggat gaaggacgac caggccttga cgcgcccaga ggccgctgag 240
cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa 300
tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctacaa ggtggatgtg 360
atccacccaa aaccgcaagg gccacctgtg gcctcctcgt cctcggccac tagcctgccg 420
tggcccgtgg tcatcgccat cccagccggc gctgtcttca tcctgggcac cctgctcctg 480
tggttttgcc aggccagaaa gaagccgtgc acccccgcgc ctgcccctcc cctgcctggg 540
caccgcccgc cggggacggc ccgcgaccgc agcggagaca aggaccttcc ctcgttggcc 600
gccctcagcg ctggccctgg tgtggggctg tgtgaggagc atgggtctcc ggcagccccc 660
cagcacttac tgggcccagg cccagttgct ggccctaagt tgtaccccaa actctacaca 720
gacatccaca cacacacaca cacacactct cacacacact cacacgtgga gggcaaggtc 780
caccagcaca tccactatca gtgctag 807

<210> 43
<211> 268
<212> PRT
<213> Human

<400> 43
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
20 25 30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
35 40 45
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
50 55 60
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
65 70 75 80
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
85 90 95
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
100 105 110
Asn Ala Thr Tyr Lys Val Asp Val Ile His Pro Lys Pro Gln Gly Pro
115 120 125
Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val
130 135 140
Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu
145 150 155 160
Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro
165 170 175
Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly
180 185 190

Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val
 195 200 205
 Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu
 210 215 220
 Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr
 225 230 235 240
 Asp Ile His Thr His Thr His Thr His Ser His Thr His Ser His Val
 245 250 255
 Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys
 260 265

<210> 44
 <211> 876
 <212> DNA
 <213> Human

<400> 44
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 ccggccgccg ccgcccgaga gcggaccctg tccaagcccg tgctcacagg cagcaccccc 120
 gtgaacacga cgggtggactt cgggggggacc acgtccttcc agtgcaagggt gcgcagcgac 180
 gtgaagccgg tgatccagtg gctgaagcgc gtggagtacg gcgccgaggg ccgccacaac 240
 tccaccatcg atgtgggagg ccagaagttt gtgggtgctgc ccacgggtga cgtgtgggtcg 300
 cggcccgcag gctcctacct caataagctg ctcacacccc gtgcccgcga ggacgatgcg 360
 ggcatgtaca tctgccttgg cgccaacacc atgggtgtaca gcttcgcgag cgccttcttc 420
 accgtgctgc cagacccaaa accgcaaggg ccacctgtgg cctcctcgtc ctcggccact 480
 agcctgcccgt ggcccgtggt catcggcatc ccagccggcg ctgtcttcat cctgggcacc 540
 ctgctcctgt ggctttgcca ggcccagaag aagccgtgca cccccgcgcc tgcccctccc 600
 ctgcctgggc accgcccgcc ggggacggcc cgcgaccgca gcggagacaa ggaccttccc 660
 tcgttggccc cctcagcgc tggccctggt gtggggctgt gtgaggagca tgggtctccg 720
 gcagcccccc agcacttact gggcccaggc ccagttgctg gccctaagtt gtaccccaaa 780
 ctctacacag acatccacac acacacacac acacactctc acacacactc acacgtggag 840
 ggcaaggtcc accagcacat ccactatcag tgctag 876

<210> 45
 <211> 291
 <212> PRT

<213> Human

<400> 45
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Glu Arg Thr Arg Ser Lys
 20 25 30
 Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly
 35 40 45
 Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val
 50 55 60
 Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn
 65 70 75 80
 Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly
 85 90 95
 Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile
 100 105 110
 Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala
 115 120 125
 Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro

130		135		140											
Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr
145				150					155						160
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe
			165						170					175	
Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro
		180						185					190		
Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly
		195					200					205			
Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala
	210					215					220				
Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro
225				230						235					240
Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys
			245						250					255	
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His
		260					265					270			
Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His
	275					280						285			
Tyr	Gln	Cys													
	290														

<210> 46

<211> 522

<212> DNA

<213> Human

<400> 46

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gccactagcc	tgccgtggcc	cgtggtcatc	ggcatcccag	ccggcgctgt	cttcacctcg	180
ggcaccctgc	tctgtgtggc	ttgccaggcc	cagaagaagc	cgtgcacccc	cgcgctgcc	240
cctcccctgc	ctgggcaccg	cccgcggggg	acggcccgcg	accgcagcgg	agacaaggac	300
cttcctcctg	tggcgcgcct	cagcgtggc	cctggtgtgg	ggctgtgtga	ggagcatggg	360
tctccggcag	ccccccagca	cttactgggc	ccaggcccag	ttgctggccc	taagttgtac	420
cccaaactct	acacagacat	ccacacacac	acacacacac	actctcacac	acactcacac	480
gtggagggca	aggtccacca	gcacatccac	tatcagtgtc	ag		522

<210> 47

<211> 173

<212> PRT

<213> Human

<400> 47

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Pro	Lys	Pro	Gln	Gly
			20					25					30		
Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val
		35					40					45			
Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu
	50					55					60				
Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala
65				70					75					80	
Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser
			85					90					95		
Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly

Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
130						135					140				
Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile
145					150					155					160
Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly
				165					170					175	
His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr
			180					185					190		
Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu
		195					200					205			
Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser
	210					215					220				
Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln
225					230					235					240
Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr
				245					250					255	
Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser
			260					265					270		
Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala
		275					280					285			
Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val
	290					295					300				
Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu
305					310					315					320
Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr
				325					330					335	
Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe
			340					345					350		
Leu	Thr	Val	Leu	Pro											
			355												

<210> 50
 <211> 718
 <212> DNA
 <213> Human

<400> 50	
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gcccggctgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg	180
accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg	240
ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag	300
gccaccaacg gcttcggcag ccttagcgtc aactacacc tcgtcgtgct ggatgacatt	360
agcccaggga aggagagcct ggggcccac agctcctctg ggggtcaaga ggacccgcc	420
agccagcagt gggcacgacc gcgcttcaca cagccctcca agatgaggcg ccgggtgatc	480
gcacggcccc tgggtagctc cgtgcggctc aagtgcgtgg ccagcgggca ccctcgcccc	540
gacatcacgt ggatgaagga cgaccaggcc ttgacgcgcc cagaggccgc tgagcccagg	600
aagaagaagt ggacactgag cctgaagaac ctgcggcccg aggacagcgg caaatacacc	660
tgccgcgtgt cgaaccgcgc gggcgccatc aacgccacct acaaggtgga tgtgatcc	718

<210> 51
 <211> 239
 <212> PRT
 <213> Human

<400> 51
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu

1	5	10	15
Gly Ala Phe	Pro Pro Ala Ala Ala	Ala Arg Gly Pro Pro	Lys Met Ala
	20	25	30
Asp Lys Val	Val Pro Arg Gln Val	Ala Arg Leu Gly Arg	Thr Val Arg
	35	40	45
Leu Gln Cys	Pro Val Glu Gly Asp	Pro Pro Pro Leu Thr	Met Trp Thr
	50	55	60
Lys Asp Gly	Arg Thr Ile His Ser	Gly Trp Ser Arg Phe	Arg Val Leu
65	70	75	80
Pro Gln Gly	Leu Lys Val Lys Gln	Val Glu Arg Glu Asp	Ala Gly Val
	85	90	95
Tyr Val Cys	Lys Ala Thr Asn Gly	Phe Gly Ser Leu Ser	Val Asn Tyr
	100	105	110
Thr Leu Val	Val Leu Asp Asp Ile	Ser Pro Gly Lys Glu	Ser Leu Gly
	115	120	125
Pro Asp Ser	Ser Ser Gly Gly Gln	Glu Asp Pro Ala Ser	Gln Gln Trp
	130	135	140
Ala Arg Pro	Arg Phe Thr Gln Pro	Ser Lys Met Arg Arg	Arg Val Ile
145	150	155	160
Ala Arg Pro	Val Gly Ser Ser Val	Arg Leu Lys Cys Val	Ala Ser Gly
	165	170	175
His Pro Arg	Pro Asp Ile Thr Trp	Met Lys Asp Asp Gln	Ala Leu Thr
	180	185	190
Arg Pro Glu	Ala Ala Glu Pro Arg	Lys Lys Lys Trp Thr	Leu Ser Leu
	195	200	205
Lys Asn Leu	Arg Pro Glu Asp Ser	Gly Lys Tyr Thr Cys	Arg Val Ser
	210	215	220
Asn Arg Ala	Gly Ala Ile Asn Ala	Thr Tyr Lys Val Asp	Val Ile
225	230	235	

<210> 52
 <211> 787
 <212> DNA
 <213> Human

<400> 52

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtg	agggggaccc	gccgccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgc	agctcctctg	ggggtcaaga	ggaccccgcc	420
agccagcagt	gggagcggac	ccgttccaag	cccgtgctca	caggcacgca	ccccgtgaac	480
acgacggtgg	acttcggggg	gaccacgtcc	ttccagtgc	aggtgcgcag	cgacgtgaag	540
ccggtgatcc	agtggctgaa	gcgcgtggag	tacggcgccg	agggccgcca	caactccacc	600
atcgaatgtg	gcggccagaa	gtttgtggtg	ctgccacagg	gtgacgtgtg	gtcgcggccc	660
gacggctcct	acctcaataa	gctgctcatc	acccgtgccc	gccaggacga	tgccgggcatg	720
tacatctgcc	ttggcgccaa	caccatgggc	tacagcttcc	gcagcgcctt	cctcaccgtg	780
ctgccag						787

<210> 53
 <211> 262
 <212> PRT
 <213> Human

<400> 53

ttccgcagcg ccttcctcac cgtgctgcc a g

991

<210> 55

<211> 330

<212> PRT

<213> Human

<400> 55

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
		50				55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
		115					120					125			
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
		130				135					140				
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
145					150				155					160	
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
				165				170						175	
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
			180				185						190		
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
		195					200					205			
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr
	210					215					220				
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln
225					230				235					240	
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg
				245					250					255	
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly
			260				265						270		
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro
		275					280					285			
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp
	290					295					300				
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser
305					310					315					320
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro						
				325					330						

<210> 56

<211> 799

<212> DNA

<213> Human

<400> 56

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ccggccgccg	ccgccccgaga	tgacattagc	ccaggggaagg	agagcctggg	gcccgcacagc	120
tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	cacgaccgcg	cttcacacag	180
ccctccaaga	tgaggcgccg	ggtgatcgca	cggcccgtgg	gtagctccgt	gcggctcaag	240
tgctgggcca	gcgggcaccc	tcggcccgcac	atcacgtgga	tgaaggacga	ccaggccttg	300
acgcgccag	aggccgctga	gcccaggaag	aagaagtgga	cactgagcct	gaagaacctg	360
cggccggagg	acagcggcaa	atacacctgc	cgcgtgtcga	accgcgcggg	cgccatcaac	420
gccacctaca	aggtggatgt	gatccagcgg	acccgttcca	agcccgtgct	cacaggcacg	480
caccccgtag	acacgacggg	ggacttcggg	gggaccacgt	ccttccagt	caaggtgcgc	540
agcgacgtga	agccggtgat	ccagtggctg	aagcgcgtgg	agtacggcgc	cgagggccgc	600
cacaactcca	ccatcgatgt	gggcggccag	aagtttgtgg	tgctgccac	gggtgacgtg	660
tggtcgcgcc	ccgacggctc	ctacctcaat	aagctgctca	tcacccgtgc	ccgccaggac	720
gatgcgggca	tgtacatctg	ccttggcgcc	aacaccatgg	gctacagctt	ccgcagcgcc	780
ttcctcaccg	tgctgccag					799

<210> 57

<211> 266

<212> PRT

<213> Human

<400> 57

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
		35					40					45			
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
	50					55					60				
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
65				70					75					80	
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
			85						90					95	
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
			100					105					110		
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
	115					120						125			
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
	130				135						140				
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr
145				150						155				160	
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln
			165						170					175	
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg
			180					185					190		
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly
	195						200					205			
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro
	210					215					220				
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp
225				230						235				240	
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser
			245						250					255	
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro						
			260					265							

<210> 58

<211> 433
 <212> DNA
 <213> Human

<400> 58
 atgacgccga gccccctgtt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
 ccggccgccg ccgcccagagg ccccccaaag atggcggaca aggtgggtccc acggcaggtg 120
 gcccggttg ggcgcactgt gcggctgcag tgcccagtgg aggggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggg tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggatgacatt 360
 agcccaggga aggagagcct ggggcccgcac agctcctctg ggggtcaaga ggaccccgcc 420
 agccagcagt ggg 433

<210> 59
 <211> 144
 <212> PRT
 <213> Human

<400> 59
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115 120 125
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140

<210> 60
 <211> 637
 <212> DNA
 <213> Human

<400> 60
 atgacgccga gccccctgtt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
 ccggccgccg ccgcccagagg ccccccaaag atggcggaca aggtgggtccc acggcaggtg 120
 gcccggttg ggcgcactgt gcggctgcag tgcccagtgg aggggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggg tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggcacgaccg 360
 cgcttcacac agccctccaa gatgaggcgc cgggtgatcg cacggcccgt gggtagctcc 420
 gtgcggtca agtgctggc cagcgggcac cctcggccc acatcacgtg gatgaaggac 480
 gaccaggcct tgacgcgccc agaggccgct gagcccagga agaagaagtg gacactgagc 540
 ctgaagaacc tgcggccgga ggacagcggc aaatacacct gccgcgtgtc gaaccgcgcg 600
 ggcgccatca acgccaccta caaggtggat gtgatcc 637

<210> 61
 <211> 212
 <212> PRT
 <213> Human

<400> 61
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 115 120 125
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 130 135 140
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 145 150 155 160
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
 165 170 175
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
 180 185 190
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
 195 200 205
 Val Asp Val Ile
 210

<210> 62
 <211> 706
 <212> DNA
 <213> Human

<400> 62
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 ccggccgccg ccgcccagg cccccaaaag atggcggaca aggtgggtccc acggcaggtg 120
 gcccggtgg ggcgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgtg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcagggggc tgaagggtgaa gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacacc tcgtcgtgct ggagcggacc 360
 cgttccaagc ccgtgctcac aggcacgcac cccgtgaaca cgacggtgga cttcgggggg 420
 accacgtcct tccagtgaag ggtgcgcagc gacgtgaagc cggatgatcca gtggctgaag 480
 cgcggtggag acggcgccga gggccgccac aactccacca tcgatgtggg cggccagaag 540
 tttgtggtgc tgcccacggg tgacgtgtgg tcgcggcccg acggctccta cctcaataag 600
 ctgctcatca cccgtgcccg ccaggacgat gcgggcatgt acatctgcct tggcgccaac 660
 accatgggct acagcttccg cagcgccttc ctcaccgtgc tgccag 706

<210> 63
 <211> 235
 <212> PRT

<213> Human

<400> 63

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1              5              10              15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20              25              30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35              40              45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50              55              60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65              70              75              80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85              90              95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100             105             110
Thr Leu Val Val Leu Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
 115             120             125
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
 130             135             140
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
 145             150             155             160
Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val
 165             170             175
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
 180             185             190
Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
 195             200             205
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
 210             215             220
Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 225             230             235
```

<210> 64

<211> 445

<212> DNA

<213> Human

<400> 64

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atgacgccga gccccctgtt gctgctcctg ctgccgccgc tgctgctggg ggccttccca      60
ccggccgccc ccgcccgaga tgacattagc ccagggaagg agagcctggg gcccacagc      120
tcctctgggg gtcaagagga ccccgccagc cagcagtggg cagcaccgcg cttcacacag      180
ccctccaaga tgaggcgccg ggtgatcgca cggcccgtgg gtagctccgt gcggctcaag      240
tgcggtggcca gcgggcaccc tcggcccgac atcacgtgga tgaaggacga ccaggccttg      300
acgcgcccag aggccgctga gcccggaag aagaagtgga cactgagcct gaagaacctg      360
cggccggagg acagcggcaa atacacctgc cgcgtgtcga accgcgcggg cgccatcaac      420
gccacctaca agtggtgatgt gatcc                                     445
```

<210> 65

<211> 148

<212> PRT

<213> Human

<400> 65

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1              5              10              15
```

Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
		35					40					45			
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
		50				55					60				
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
65					70					75					80
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
				85					90					95	
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
			100					105					110		
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
		115					120					125			
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
		130				135					140				
Val	Asp	Val	Ile												
145															

<210> 66
 <211> 514
 <212> DNA
 <213> Human

<400> 66	
atgacgccga gccccctgtt gctgctcctg ctgccgccgc tgctgctggg ggccttccca	60
ccggccgccg ccgcccagaga tgacattagc ccaggaagg agagcctggg gcccacagc	120
tcctctgggg gtcaagagga ccccgccagc cagcagtggg agcggaccg ttccaagccc	180
gtgctcacag gcacgcaccc cgtgaacacg acggtggact tcggggggac cacgtccttc	240
cagtgaagg tgccgcagcga cgtgaagccg gtgatccagt ggctgaagcg cgtggagtac	300
ggcgccgagg gccgccacaa ctccaccatc gatgtgggcg gccagaagt tgtggtgctg	360
cccacgggtg acgtgtggtc gcggcccgc ggctcctacc tcaataagct gctcatcacc	420
cgtgcccgcc aggacgatgc gggcatgtac atctgccttg gcgccaacac catgggctac	480
agcttccgca gcgccttcct caccgtgctg ccag	514

<210> 67
 <211> 171
 <212> PRT
 <213> Human

<400> 67	
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu	
1	5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly	
	20 25 30
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro	
	35 40 45
Ala Ser Gln Gln Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly	
	50 55 60
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe	
65	70 75 80
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys	
	85 90 95
Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val	
	100 105 110
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg	
	115 120 125

Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
	130					135					140				
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
145					150					155					160
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro					
				165					170						

<210> 68
 <211> 718
 <212> DNA
 <213> Human

<400> 68

atgacgccga	gccccctgtt	gctgctcctg	ctgccgccgc	tgctgctggg	ggccttccca	60
ccggccgccg	ccgcccagac	acgaccgcgc	ttcacacagc	cctccaagat	gaggcgccgg	120
gtgatcgcac	ggcccgtggg	tagctccgtg	cggctcaagt	gcgtggccag	cgggcaccct	180
cgggccgaca	tcacgtggat	gaaggacgac	caggccttga	cgcgcccaga	ggccgctgag	240
cccaggaaga	agaagtggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacctgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacg	ccacctacaa	ggtggatgtg	360
atccagcgga	cccgttccaa	gcccgtgctc	acaggcacgc	accccgtgaa	cacgacggtg	420
gacttcgggg	ggaccacgtc	cttccagtgc	aaggtgcgca	gcgacgtgaa	gccggtgatc	480
cagtggctga	agcgcgtgga	gtacggcgcc	gagggccgcc	acaactccac	catcgatgtg	540
ggcggccaga	agtttgtggt	gctgcccacg	ggtgacgtgt	ggtcgcggcc	cgacggctcc	600
tacctcaata	agctgtcat	caccctgccc	cgccaggacg	atgcgggcat	gtacatctgc	660
cttggcgcca	acaccatggg	ctacagcttc	cgcagcgctt	tcctcaccgt	gctgccag	718

<210> 69
 <211> 239
 <212> PRT
 <213> Human

<400> 69

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr
			20					25					30		
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser
		35					40					45			
Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile
	50					55					60				
Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu
65					70					75					80
Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu
				85					90					95	
Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile
			100					105					110		
Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro
		115					120					125			
Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly
	130					135					140				
Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile
145					150					155					160
Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser
				165					170					175	
Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp
			180					185					190		
Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr

	195		200		205
Arg	Ala Arg Gln Asp Asp	Ala Gly Met Tyr Ile	Cys Leu Gly Ala Asn		
210		215	220		
Thr	Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro				
225		230	235		

<210> 70
 <211> 352
 <212> DNA
 <213> Human

<400> 70
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 ccggccgccg ccgcccagagg ccccccaaag atggcggaca aggtggtccc acggcaggtg 120
 gcccggtgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgtg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgctgtgctg 240
 ccgcaggggc tgaagggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gtttcggcag ccttagcgtc aactacaccc tcgtcgtgct gg 352

<210> 71
 <211> 117
 <212> PRT
 <213> Human

<400> 71
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu
 115

<210> 72
 <211> 160
 <212> DNA
 <213> Human

<400> 72
 atgacgccga gccccctgtt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
 ccggccgccg ccgcccagaga tgacattagc ccagggaagg agagcctggg gcccgacagc 120
 tcctctgggg gtcaagagga ccccgccagc cagcagtggg 160

<210> 73
 <211> 53
 <212> PRT
 <213> Human

<400> 73

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1          5          10          15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
          20          25          30
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
          35          40          45
Ala Ser Gln Gln Trp
          50
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<210> 74

<211> 364

<212> DNA

<213> Human

<400> 74

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ccggccgccg ccgcccagag acgaccgcgc ttcacacagc cctccaagat gaggcgccgg      120
gtgatcgcac ggcccggtgg tagctccgtg cggctcaagt gcgtggccag cgggcaccct      180
cggcccgaca tcacgtggat gaaggacgac caggccttga cgcgcccaaga ggccgctgag      240
cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa      300
tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctacaa ggtggatgtg      360
atcc                                             364
```

<210> 75

<211> 121

<212> PRT

<213> Human

<400> 75

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1          5          10          15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
          20          25          30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
          35          40          45
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
          50          55          60
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
          65          70          75          80
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
          85          90          95
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
          100          105          110
Asn Ala Thr Tyr Lys Val Asp Val Ile
          115          120
```

<210> 76

<211> 433

<212> DNA

<213> Human

<400> 76

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atgacgccga gccccctgtt gctgctcctg ctgccgccgc tgctgctggg ggccttccca      60
ccggccgccg ccgcccagaga gcggaccctt tccaagcccg tgctcacagg cagcaccccc      120
gtgaacacga cggtggactt cgggggggacc acgtccttcc agtgcaaggt gcgcagcgac      180
gtgaagcccg tgatccagtg gctgaagcgc gtggagtacg gcgccgaggg ccgccacaa      240
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tccaccatcg atgtgggagg ccagaagttt gtgggtgctgc ccacgggtga cgtgtgggtcg 300
 cggcccgacg gctcctacct caataagctg ctcataccccc gtgcccggcca ggacgatgcg 360
 ggcattgtaca tctgccttgg cgccaacacc atggggtaca gcttccgcag cgccttcctc 420
 accgtgctgc cag 433

<210> 77
 <211> 144
 <212> PRT
 <213> Human

<400> 77
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Glu Arg Thr Arg Ser Lys
 20 25 30
 Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly
 35 40 45
 Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val
 50 55 60
 Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn
 65 70 75 80
 Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly
 85 90 95
 Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile
 100 105 110
 Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala
 115 120 125
 Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
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<210> 78
 <211> 79
 <212> DNA
 <213> Human

<400> 78
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<210> 79
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 <212> PRT
 <213> Human

<400> 79
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 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg
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<210> 80
 <211> 1590
 <212> DNA
 <213> Mouse

<400> 80
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<210> 81

<211> 529

<212> PRT

<213> Mouse

<400> 81

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
			20				25					30		Val
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35				40						45		Pro
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
	50					55					60			Arg
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
				85				90						95
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
			100					105					110	Ile
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly
		115					120					125		Ser
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro
		130					135				140			Arg
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro
145					150					155				160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg
				165						170				175
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu
			180					185						190

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<210> 83
 <211> 411
 <212> PRT
 <213> Mouse

<400> 83

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20				25					30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
			35				40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
			50			55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65				70				75						80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
			85					90					95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
			100					105					110		
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
			115				120					125			
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
			130				135				140				
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
145				150						155				160	
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
			165					170					175		
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
			180					185					190		
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
			195				200					205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
			210				215					220			
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro	Pro
225				230						235				240	
Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro
			245					250					255		
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val
			260					265					270		
Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser

275	280	285
Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly	Thr Ser Arg Glu Arg	
290	295	300
Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val	Gly Ile Cys Glu Glu	
305	310	315
His Gly Ser Ala Met Ala Pro Gln His Ile Leu	Ala Ser Gly Ser Thr	
325	330	335
Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr	Asp Val His Thr His	
340	345	350
Thr His Thr His Thr Cys Thr His Thr Leu Ser	Cys Gly Gly Gln Gly	
355	360	365
Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu	Asn Thr Ala Asn Leu	
370	375	380
Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly	Pro Arg Gln Gln Val	
385	390	395
Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser		400
405	410	

<210> 84
 <211> 1305
 <212> DNA
 <213> Mouse

<400> 84

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<210> 85
 <211> 434
 <212> PRT
 <213> Mouse

<400> 85

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
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Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
20 25 30

<213> Mouse

<400> 86

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<210> 87

<211> 502

<212> PRT

<213> Mouse

<400> 87

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
		20					25				30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35					40				45			Pro
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
		50				55					60			Arg
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
				85				90						95
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
									105				110	Ile
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg
														Val
		115					120					125		
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala
							135					140		Ser
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr
														Leu
		145			150				155					160
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu
														Ser

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<210> 89

<211> 438

<212> PRT

<213> Mouse

<400> 89

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20				25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln
			35				40					45		
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Val
			50				55				60			
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala
65					70					75				80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr
				85					90				95	Leu
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu
			100					105					110	Ser
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg
		115					120					125		Val
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val
		130				135					140			Ile
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val
145					150					155				160
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
				165					170					175
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr
			180					185					190	Gly
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
		195					200					205		Phe
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
		210				215					220			Tyr
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
225					230					235				240
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser
				245					250					255
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met
			260					265					270	Ala
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly
													Ile	

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ggttcatcaa	caccagcatg	tccactatca	gtgctaaata	cagcgaatct	ccaagcactg	1080
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ggaagagtat	cttag					1155

<210> 93
 <211> 384
 <212> PRT
 <213> Mouse

<400> 93

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val	
			20				25						30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro	
		35					40					45				
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	
	50					55					60					
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu	
65					70				75						80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys	
				85					90					95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile	
			100					105					110			
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	
			115				120					125				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	
	130					135					140					
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	
145					150					155					160	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	
				165					170					175		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	
			180				185						190			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	
	195						200					205				
His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	
	210					215					220					
Ser	Leu	Pro	Trp	Pro	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe		
225					230					235				240		
Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	
				245					250					255		
Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	
			260					265					270			
Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	
			275				280					285				
Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	
	290					295					300					
Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	
305					310					315					320	
Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	
				325					330					335		
Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	
			340					345				350				
Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	

355 360 365
 Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser
 370 375 380

<210> 94
 <211> 1224
 <212> DNA
 <213> Mouse

<400> 94
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 cgactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctcg 240
 aagtggaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg agcggactcg ttccaagcct 360
 gtgctcacag ggacacaccc tgtgaacaca acggtggact tcggtgggac aacgtccttc 420
 cagtgaagg tgccgagtga cgtgaagcct gtgatccagt ggctgaagcg ggtggagtac 480
 ggctccgagg gacgccacaa ctccaccatt gatgtgggtg gccagaagtt tgtgggtgtg 540
 cccacgggtg atgtgtggtc acggcctgat ggctcctacc tcaacaagct gctcatctct 600
 cgggcccgcc aggatgatgc tggcatgtac atctgcctag gtgcaaatac catgggctac 660
 agtttccgta gcgccttcct cactgtatta ccagaccca aacctccagg gcctcctatg 720
 gcttcttcat cgtcatccac aagcctgcc tggcctgtgg tgatcgcat cccagctggg 780
 gctgtcttca tcctaggcac tgtgctgctc tggctttgcc agaccaagaa gaagccatgt 840
 gcccagcat ctacacttcc tgtgcctggg catcgtcccc caggacatc ccgagaacgc 900
 agtggtgaca aggacctgcc ctcatgggt gtgggcatat gtgaggagca tggatccgcc 960
 atggcccccc agcacatcct ggctctggc tcaactgctg gcccgaagct gtacccaag 1020
 ctatacacag atgtgcacac acacacacat acacacacct gcactcacac gctctcatgt 1080
 ggagggcaag gttcatcaac accagcatgt ccactatcag tgctaaatac agcgaatctc 1140
 caagcactgt gtcctgaggt aggcatttgg gggccaaggc aacagggttg gagaattgag 1200
 aacaatggag gaagagtatc ttag 1224

<210> 95
 <211> 407
 <212> PRT
 <213> Mouse

<400> 95
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val
 115 120 125
 Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val
 130 135 140
 Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr

145		150		155		160
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys						
	165		170		175	
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser						
	180		185		190	
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly						
	195		200		205	
Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser						
	210		215		220	
Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met						
225	230		235		240	
Ala Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly						
	245		250		255	
Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu						
	260		265		270	
Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val						
	275		280		285	
Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys						
	290		295		300	
Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala						
305	310		315		320	
Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys						
	325		330		335	
Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His His						
	340		345		350	
Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro						
	355		360		365	
Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys						
	370		375		380	
Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu						
385	390		395		400	
Asn Asn Gly Gly Arg Val Ser						
	405					

<210> 96
 <211> 963
 <212> DNA
 <213> Mouse

<400> 96						
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aggcgccgag	tgattgcacg	gcctgtgggt	agctctgtgc	ggctcaagtg	tgtggccagt	240
gggcacccac	ggccagacat	catgtgggat	aaggatgacc	agaccttgac	gcattctagag	300
gctagtgaac	acagaaagaa	gaagtggaca	ctgagcttga	agaacctgaa	gcctgaagac	360
agtggcaagt	acacgtgccg	tgtatctaac	aaggccgggtg	ccatcaacgc	cacctacaaa	420
gtggatgtaa	tccaccccaa	acctccaggg	cctcctatgg	cttcttcatc	gtcatccaca	480
agcctgccat	ggcctgtggg	gatcggcatc	ccagctgggtg	ctgtcttcat	cctaggcact	540
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tcattggctg	tgggcatatg	tgaggagcat	ggatccgcca	tggcccccca	gcacatcctg	720
gcctctggct	caactgctgg	ccccaaagctg	taccccaagc	tatacacaga	tgtgcacaca	780
cacacacata	cacacacctg	cactcacacg	ctctcatgtg	gagggcaagg	ttcatcaaca	840
ccagcatgtc	cactatcagt	gctaaatata	gcgaatctcc	aagcactgtg	tcctgaggta	900
ggcatttggg	ggccaaggca	acaggttggg	agaattgaga	acaatggagg	aagagtatct	960
tag						963

<210> 97
 <211> 320
 <212> PRT
 <213> Mouse

<400> 97
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
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 20 25 30
 Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
 35 40 45
 Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
 50 55 60
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
 65 70 75 80
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
 85 90 95
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
 100 105 110
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
 115 120 125
 Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
 130 135 140
 His Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Thr
 145 150 155 160
 Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe
 165 170 175
 Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro
 180 185 190
 Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly
 195 200 205
 Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val
 210 215 220
 Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile Leu
 225 230 235 240
 Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr
 245 250 255
 Asp Val His Thr His Thr His Thr His Thr Cys Thr His Thr Leu Ser
 260 265 270
 Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu
 275 280 285
 Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly
 290 295 300
 Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser
 305 310 315 320

<210> 98
 <211> 1032
 <212> DNA
 <213> Mouse

<400> 98
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 gcgcgagatg atattagttcc agggaaggag agccctgggc caggtgggttc ttcggggggc 120
 caggaggacc cagccagcca gcagtgggag cggactcgtt ccaagcctgt gctcacaggg 180

acacaccctg	tgaacacaac	ggtggacttc	ggtgggacaa	cgtccttcca	gtgcaaggtg	240
cgcagtgcg	tgaagcctgt	gatccagtgg	ctgaagcggg	tggagtacgg	ctccgagggg	300
cgccacaact	ccaccattga	tgtgggtggc	cagaagtttg	tgggtgtgcc	cacgggtgat	360
gtgtggtcac	ggcctgatgg	ctcctacctc	aacaagctgc	tcatctctcg	ggcccgccag	420
gatgatgctg	gcatgtacat	ctgcctaggt	gcaaatacca	tgggctacag	tttccgtagc	480
gccttcctca	ctgtattacc	agaccccaaa	cctccagggc	ctcctatggc	ttcttcatcg	540
tcatccacaa	gcctgccatg	gcctgtgggtg	atcggcattcc	cagctgggtgc	tgtcttcatc	600
ctaggcactg	tgctgctctg	gctttgccag	accaagaaga	agccatgtgc	cccagcatct	660
acacttcctg	tgcttgggca	tcgtccccc	gggacatccc	gagaacgcag	tggtgacaag	720
gacctgccct	cattggctgt	gggcatatgt	gaggagcatg	gatccgccat	ggccccccag	780
cacatcctgg	cctctggctc	aactgctggc	cccaagctgt	accccaagct	atacacagat	840
gtgcacacac	acacacatac	acacacctgc	actcacacgc	tctcatgtgg	agggcaaggt	900
tcatcaacac	cagcatgtcc	actatcagtg	ctaaatacag	cgaatctcca	agcactgtgt	960
cctgaggtag	gcatttgggg	gccaaaggcaa	caggttggga	gaattgagaa	caatggagga	1020
agagtatctt	ag					1032

<210> 99

<211> 343

<212> PRT

<213> Mouse

<400> 99

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10					15	
Ser	Ala	Glu	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20				25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln
			35				40					45		
Trp	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro
						55					60			
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys
65					70					75				80
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu
				85				90						95
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln
			100					105					110	
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly
			115				120					125		
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala
	130					135					140			
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg
145				150						155				160
Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro
				165					170					175
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile
			180					185					190	
Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp
		195					200						205	
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro
	210					215					220			
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp
225					230					235				240
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser
				245					250					255
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro
			260					265					270	
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr


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cccaagctat acacagatgt gcacacacac acacatacac acacctgcac tcacacgctc 720
tcatgtggag ggcaagggtc atcaacacca gcatgtccac tatcagtgtc aaatacagcg 780
aatctccaag cactgtgtcc tgaggtaggc atttgggggc caaggcaaca ggttgggaga 840
attgagaaca atggaggaag agtatcttag 870

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<210> 103
 <211> 289
 <212> PRT
 <213> Mouse

<400> 103

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20					25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
		35					40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65				70					75					80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
			85					90					95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
		100					105						110		
Met	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser
	115					120						125			
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val
	130					135					140				
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys
145				150					155					160	
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro
			165				170						175		
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala
		180					185					190			
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile
	195					200					205				
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
	210				215						220				
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu
225				230					235					240	
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val
			245					250					255		
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp
	260					265					270				
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val
	275					280					285				

Ser

<210> 104
 <211> 678
 <212> DNA
 <213> Mouse

<400> 104

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tcatcgtcat	ccacaagcct	gccatggcct	gtggtgatcg	gcatcccagc	tggtgctgtc	240
ttcatcctag	gcaactgtgt	gctctggctt	tgccagacca	agaagaagcc	atgtgcccc	300
gcatctacac	ttcctgtgcc	tgggcatcgt	cccccagga	catcccagga	acgcagtgg	360
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acagatgtgc	acacacacac	acatacacac	acctgcactc	acacgctctc	atgtggaggg	540
caagggttcat	caacaccagc	atgtccacta	tcagtgtctaa	atacagcgaa	tctccaagca	600
ctgtgtcctg	aggtaggcat	ttggggggcca	aggcaacagg	ttgggagaat	tgagaacaat	660
ggaggaagag	tatcttag					678

<210> 105

<211> 225

<212> PRT

<213> Mouse

<400> 105

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20				25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln
			35				40					45		
Trp	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser
			50			55					60			
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala
65					70				75					80
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys
				85					90				95	
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro
			100					105				110		
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu
			115				120				125			
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His
			130			135					140			
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu
145					150				155				160	
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr
				165					170				175	
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser
			180					185				190		
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile
			195			200					205			
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg
			210			215					220			
Ser														
225														

<210> 106

<211> 882

<212> DNA

<213> Mouse

<400> 106

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cctgtgggta	gctctgtgcg	gctcaagtgt	gtggccagt	ggcaccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaaagaag	240
aagtggacac	tgagcttgaa	gaacctgaag	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccggtgc	catcaacgcc	acctacaaa	tgatgtaat	ccacccaaa	360
cctccagggc	ctcctatggc	ttcttcatcg	tcatccacaa	gcctgccatg	gcctgtggtg	420
atcggcatcc	cagctggtgc	tgtcttcatc	ctaggcactg	tgctgctctg	gctttgccag	480
accaagaaga	agccatgtgc	cccagcatct	acacttcctg	tgctgggca	tcgtcccca	540
gggacatccc	gagaacgcag	tggtgacaag	gacctgccct	cattggctgt	gggcatatgt	600
gaggagcatg	gatccgccat	ggccccccag	cacatcctgg	cctctggctc	aactgctggc	660
cccaagctgt	accccaagct	atacacagat	gtgcacacac	acacacatac	acacacctgc	720
actcacacgc	tctcatgtgg	agggcaaggt	tcatcaacac	cagcatgtcc	actatcagt	780
ctaaatacag	cgaatctcca	agcactgtgt	cctgaggtag	gcatttgggg	gccaaggcaa	840
caggttgagg	gaattgagaa	caatggagga	agagtatctt	ag		882

<210> 107

<211> 293

<212> PRT

<213> Mouse

<400> 107

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10					15	
Ser	Ala	Glu	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys
			20				25					30		
Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg
			35				40					45		
Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met
	50					55				60				Lys
Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys
65					70				75					80
Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly
			85					90						95
Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr
			100					105					110	Tyr
Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala
		115					120					125		Ser
Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile
	130					135					140			Pro
Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys
145					150				155					160
Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro
				165				170						175
His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp
			180					185					190	Leu
Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met
		195					200					205		Ala
Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu
	210					215					220			Tyr
Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr
225					230				235					240
Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala
				245					250					255
Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro
			260					265					270	Glu
Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn
		275					280						285	Asn
Gly	Gly	Arg	Val	Ser										

<210> 108

<211> 951

<212> DNA

<213> Mouse

<400> 108

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atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgagagc ggactcgttc caagcctgtg ctcacaggga cacaccctgt gaacacaacg     120
gtggacttcg gtgggacaac gtccttccag tgcaagggtg gcagtgacgt gaagcctgtg     180
atccagtggc tgaagcgggt ggagtacggc tccgaggggac gccacaactc caccattgat     240
gtgggtggcc agaagtttgt ggtgttgccc acgggtgatg tgtggtcacg gcctgatggc     300
tcctacctca acaagctgct catctctcgg gcccgccagg atgatgctgg catgtacatc     360
tgcctagggtg caaataccat gggctacagt ttccgtagcg ccttcctcac tgtattacca     420
gaccccaaac ctccagggcc tcctatggct tcttcatcgt catccacaag cctgccatgg     480
cctgtggtga tcggcatccc agctggtgct gtcttcatcc taggcactgt gctgctctgg     540
ctttgccaga ccaagaagaa gccatgtgcc ccagcatcta cacttcctgt gcctgggcat     600
cgtccccccg ggacatcccc agaacgcagt ggtgacaagg acctgccctc attggctgtg     660
ggcatatgtg aggagcatgg atccgccatg gccccccagc acatcctggc ctctgggtca     720
actgctggcc ccaagctgta cccaagcta tacacagatg tgcacacaca cacacatata     780
cacacctgca ctcacacgct ctcatgtgga gggcaagggt catcaacacc agcatgtcca     840
ctatcagtg c taaatacagc gaatctccaa gcaactgtgtc ctgaggtagg catttggggg     900
ccaaggcaac aggttgggag aattgagaac aatggaggaa gagtatctta g          951

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<210> 109

<211> 316

<212> PRT

<213> Mouse

<400> 109

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Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
Ser Ala Glu Ala Ala Arg Glu Arg Thr Arg Ser Lys Pro Val Leu Thr
          20          25          30
Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser
          35          40          45
Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu

          50          55          60
Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp
65          70          75          80
Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser
          85          90          95
Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg
          100          105          110
Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
          115          120          125
Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro
          130          135          140
Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp
145          150          155          160
Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr
          165          170          175
Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala
          180          185          190
Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu

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195	200	205
Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu		
210	215	220
Glu His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser		
225	230	235
Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr		
245	250	255
His Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln		
260	265	270
Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn		
275	280	285
Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln		
290	295	300
Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser		
305	310	315

<210> 110
 <211> 597
 <212> DNA
 <213> Mouse

<400> 110	
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg	60
gcgcgagacc ccaaacctcc agggcctcct atggcttctt catcgatcatc cacaagcctg	120
ccatggcctg tggtgatcgg catcccagct ggtgctgtct tcatcctagg cactgtgctg	180
ctctggcttt gccagaccaa gaagaagcca tgtgccccag catctacact tcctgtgcct	240
gggcatcgtc ccccaggac atccccgagaa cgagtggtg acaaggacct gccctcattg	300
gctgtgggca tatgtgagga gcatggatcc gccatggccc cccagcacat cctggcctct	360
ggctcaactg ctggcccaaa gctgtacccc aagctataca cagatgtgca cacacacaca	420
catacacaca cctgcactca cagctctca tgtggagggc aaggttcatc aacaccagca	480
tgtccactat cagtgtctaaa tacagcgaat ctccaagcac tgtgtcctga ggtaggcatt	540
tgggggcaaa ggcaacaggt tgggagaatt gagaacaatg gaggaagagt atcttag	597

<210> 111
 <211> 198
 <212> PRT

<213> Mouse

<400> 111	
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1	15
Ser Ala Glu Ala Ala Arg Asp Pro Lys Pro Pro Gly Pro Pro Met Ala	
20	30
Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile	
35	45
Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys	
50	60
Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro	
65	80
Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp	
85	95
Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met	
100	110
Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu	
115	125
Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His Thr	

130		135		140
Cys Thr His Thr Leu Ser	Cys Gly Gly Gln Gly	Ser Ser Thr Pro Ala		
145	150	155	160	
Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro				
	165	170	175	
Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn				
	180	185	190	
Asn Gly Gly Arg Val Ser				
195				

<210> 112
 <211> 1060
 <212> DNA
 <213> Mouse

<400> 112

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaag	360
gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tcgggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcatcta	gaggctagtg	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatccagcg	gactcggttc	720
aagcctgtgc	tcacaggggac	acaccctgtg	aacacaacgg	tggacttcgg	tgggacaacg	780
tccttccagt	gcaaggtgcg	cagtgcgtg	aagcctgtga	tccagtggct	gaagcgggtg	840
gagtacggct	ccgaggggacg	ccacaactcc	accattgatg	tgggtggcca	gaagtttgtg	900
gtgttgccca	cgggtgatgt	gtggtcacgg	cctgatggct	cctacctcaa	caagctgctc	960
atctctcggg	cccgccagga	tgatgctggc	atgtacatct	gcctaggtgc	aaataccatg	1020
ggctacagtt	tccgtagcgc	cttcctcact	gtattaccag			1060

<210> 113
 <211> 353
 <212> PRT
 <213> Mouse

<400> 113

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1	5
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
20	25
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	
35	40
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg	
50	55
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu	
65	70
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys	
85	90
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile	
100	105
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser	
115	120
	125

Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
130						135					140				
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
145					150					155					160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
			165					170						175	
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
		180						185					190		
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
		195					200					205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
	210					215					220				
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser
225					230					235					240
Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe
			245						250					255	
Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro
		260						265					270		
Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His
		275					280					285			
Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr
	290					295				300					
Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu
305					310					315					320
Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly
			325					330						335	
Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu
		340						345					350		
Pro															

<210> 114
 <211> 706
 <212> DNA
 <213> Mouse

<400> 114	
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg	60
gcgcgaggac ccccaagaat ggcagacaaa gtggtcccac ggcaggtggc ccgcctgggc	120
cgcactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc	180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg	240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc	300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccaggggaag	360
gagagccctg ggccaggtgg ttcttcgggg ggccaggagg acccagccag ccagcagtgg	420
gcacggcctc gcttcacaca gccctccaag atgaggcgcc gagtgattgc acggcctgtg	480
ggtagctctg tgcggctcaa gtgtgtggcc agtgggcacc cacggccaga catcatgtgg	540
atgaaggatg accagacctt gacgcactca gaggctagtg aacacagaaa gaagaagtgg	600
acactgagct tgaagaacct gaagcctgaa gacagtggca agtacacgtg ccgtgtatct	660
aacaaggccg gtgccatcaa cgccacctac aaagtggatg taatcc	706

<210> 115
 <211> 235
 <212> PRT
 <213> Mouse

<400> 115
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro

- 69 -

gatgctggca tgtacatctg cctaggtgca aataccatgg gctacagttt ccgtagcgcc
 ttctctactg tattaccag

960
 979

<210> 119
 <211> 326
 <212> PRT
 <213> Mouse

<400> 119
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45

 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
 115 120 125
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
 130 135 140
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
 145 150 155 160
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
 165 170 175
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
 180 185 190
 Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
 195 200 205
 Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
 210 215 220
 Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
 225 230 235 240
 Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
 245 250 255
 Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
 260 265 270
 Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
 275 280 285
 Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met
 290 295 300
 Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
 305 310 315 320
 Phe Leu Thr Val Leu Pro
 325

<210> 120
 <211> 787
 <212> DNA
 <213> Mouse

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<400> 120
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgagatg atattagtcc aggggaaggag agccctgggc caggtgggtc ttcggggggc      120
caggaggacc cagccagcca gcagtgggca cggcctcgct tcacacagcc ctccaagatg      180
aggcgccgag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt      240
gggcacccac ggccagacat catgtggatg aaggatgacc agaccttgac gcatctagag      300
gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac      360
agtggcaagt acacgtgccg tgtatctaac aaggccggtg ccatcaacgc cacctacaaa      420
gtggatgtaa tccagcggac tcgttccaag cctgtgctca caggacaca ccctgtgaac      480
acaacggtgg acttcggtgg gacaacgtcc ttccagtgcg aggtgcgcag tgacgtgaag      540
cctgtgatcc agtggctgaa gcgggtggag tacggctccg agggacgccg caactccacc      600
attgatgtgg gtggccagaa gtttgtgggt ttgccacggg gtgatgtgtg gtcacggcct      660
gatggctcct acctcaacaa gctgctcatc tctcggggcc gccaggatga tgctggcatg      720
tacatctgcc taggtgcaaa taccatgggc tacagtttcc gtagcgcctt cctcactgta      780
ttaccag                                           787

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<210> 121
<211> 262
<212> PRT
<213> Mouse

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<400> 121
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1              5              10              15
Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro
      20              25              30
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
      35              40              45
Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
 50              55              60
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
65              70              75              80
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
      85              90              95
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
      100             105             110
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
      115             120             125
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
      130             135             140
Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
145             150             155             160
Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
      165             170             175
Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
      180             185             190
Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
      195             200             205
Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
      210             215             220
Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met
225             230             235             240
Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
      245             250             255
Phe Leu Thr Val Leu Pro
      260

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<210> 122
 <211> 421
 <212> DNA
 <213> Mouse

<400> 122
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctgggc 120
 cgactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg 240
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccaggggaag 360
 gagagccctg ggccaggtgg ttcttcgggg ggccaggagg acccagccag ccagcagtgg 420
 g 421

<210> 123
 <211> 140
 <212> PRT
 <213> Mouse

<400> 123
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
 115 120 125
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140

<210> 124
 <211> 625
 <212> DNA
 <213> Mouse

<400> 124
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctgggc 120
 cgactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg 240
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg caccggcctc cttcacacag 360
 ccctccaaga tgaggcgccg agtgattgca cggcctgtgg gtagctctgt gcggctcaag 420
 tgtgtggcca gtgggcaccc acggccagac atcatgtgga tgaaggatga ccagaccttg 480
 acgcatctag aggctagtga acacagaaag aagaagtgga cactgagctt gaagaacctg 540
 aagcctgaag acagtggcaa gtacacgtgc cgtgtatcta acaaggccgg tgccatcaac 600

gccacctaca aagtggatgt aatcc

625

<210> 125

<211> 208

<212> PRT

<213> Mouse

<400> 125

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5					10					15	
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20					25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
		35					40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
		50				55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65					70				75						80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
				85				90						95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
			100					105					110		
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
		115					120					125			
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
		130				135					140				
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
145					150				155						160
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
				165				170					175		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
			180				185					190			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
		195					200					205			

<210> 126

<211> 694

<212> DNA

<213> Mouse

<400> 126

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccagaat	ggcagacaaa	gtggtccac	ggcaggtggc	ccgcctgggc	120
cgactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	agcggactcg	ttccaagcct	360
gtgctcacag	ggacacaccc	tgtgaacaca	acggtggact	tcggtgggac	aacgtccttc	420
cagtgaagg	tgcgcagtga	cgtgaagcct	gtgatccagt	ggctgaagcg	ggtggagtac	480
ggctccgagg	gacgccacaa	ctccaccatt	gatgtgggtg	gccagaagtt	tgtgggtgtg	540
cccacgggtg	atgtgtggtc	acggcctgat	ggctcctacc	tcaacaagct	gctcatctct	600
cgggcccgcc	aggatgatgc	tggcatgtac	atctgcctag	gtgcaaatac	catgggctac	660
agtttccgta	gcgccttcct	cactgtatta	ccag			694

<210> 127

<211> 231

<212> PRT

<213> Mouse

<400> 127

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5					10					15	
Ser	Ala	Glu	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val	
			20				25					30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
			35				40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
			50			55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65					70				75						80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
				85					90					95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
			100					105					110		
Met	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val
			115				120					125			
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
			130			135					140				
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr
145					150				155						160
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
				165					170					175	
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
			180					185					190		
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
		195					200					205			
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser
	210					215					220				
Ala	Phe	Leu	Thr	Val	Leu	Pro									
225					230										

<210> 128

<211> 433

<212> DNA

<213> Mouse

<400> 128

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgagatg	atattagtcc	aggaaggag	agccctgggc	caggtgggtc	ttcggggggc	120
caggaggacc	cagccagcca	gcagtgggca	cggcctcgct	tcacacagcc	ctccaagatg	180
aggcgccgag	tgattgcacg	gcctgtgggt	agctctgtgc	ggctcaagtg	tgtggccagt	240
gggcacccac	ggccagacat	catgtggatg	aaggatgacc	agaccttgac	gcatctagag	300
gctagtgaac	acagaaagaa	gaagtggaca	ctgagcttga	agaacctgaa	gcctgaagac	360
agtggaagt	acacgtgccg	tgtatctaac	aaggccggtg	ccatcaacgc	cacctacaaa	420
gtggatgtaa	tcc					433

<210> 129

<211> 144

<212> PRT

<213> Mouse

<400> 129

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5					10				15	

Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
		35					40					45			
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
	50					55					60				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
65					70					75					80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
				85					90					95	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
			100					105					110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
		115					120					125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
	130					135					140				

<210> 130
 <211> 502
 <212> DNA
 <213> Mouse

<400> 130	
atgacgcgga	gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
gcgcgagatg	atattagtcc agggaaggag agccctgggc caggtgggtc ttcggggggc 120
caggaggacc	cagccagcca gcagtgggag cggactcggt ccaagcctgt gctcacaggg 180
acacaccctg	tgaacacaac ggtggacttc ggtgggacaa cgtccttcca gtgcaagggtg 240
cgcagtgcg	tgaagcctgt gatccagtgg ctgaagcggg tggagtacgg ctccgaggga 300
cgccacaact	ccaccattga tgtgggtggc cagaagtttg tgggtgttgcc cacgggtgat 360
gtgtgggtcac	ggcctgatgg ctctacctc aacaagctgc tcatctctcg ggcccgccag 420
gatgatgctg	gcatgtacat ctgcctaggt gcaaatacca tgggctacag tttccgtagc 480
gccttcctca	ctgtattacc ag 502

<210> 131
 <211> 167
 <212> PRT
 <213> Mouse

<400> 131	
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1	5 10 15
Ser Ala Glu Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro	
	20 25 30
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln	
	35 40 45
Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val	
	50 55 60
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val	
65	70 75 80
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr	
	85 90 95
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys	
	100 105 110
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser	
	115 120 125
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly	
	130 135 140

Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
	210					215					220				
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro					
225					230					235					

<210> 134
 <211> 340
 <212> DNA
 <213> Mouse

<400> 134
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgaggac cccaagaat ggcagacaaa gtgggtccac ggcaggtggc ccgcctgggc 120
 cgactgtgc ggctacagtg ccagtgagg ggggaccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctctg 240
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg 340

<210> 135
 <211> 113
 <212> PRT
 <213> Mouse

<400> 135
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met

<210> 136
 <211> 148
 <212> DNA
 <213> Mouse

<400> 136
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgagatg atattagtcc aggggaaggag agccctgggc caggtggttc ttcggggggc 120
 caggaggacc cagccagcca gcagtggg 148

<210> 137
 <211> 49
 <212> PRT
 <213> Mouse

<400> 137

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro
 20 25 30
 Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
 35 40 45
 Trp

<210> 138
 <211> 352
 <212> DNA
 <213> Mouse

<400> 138
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgagcac ggctcgcgtt cacacagccc tccaagatga ggcgccgagt gattgcacgg 120
 cctgtgggta gctctgtgcg gctcaagtgt gtggccagtg ggcacccacg gccagacatc 180
 atgtggatga aggatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag 240
 aagtggacac tgagcttgaa gaacctgaag cctgaagaca gtggcaagta cacgtgccgt 300
 gtatctaaca aggccggtgc catcaacgcc acctacaaag tggatgtaat cc 352

<210> 139
 <211> 117
 <212> PRT
 <213> Mouse

<400> 139

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys
 20 25 30
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu
 35 40 45
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys
 50 55 60
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys
 65 70 75 80
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys
 85 90 95
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr
 100 105 110
 Lys Val Asp Val Ile
 115

<210> 140
 <211> 421
 <212> DNA
 <213> Mouse

<400> 140
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgagagc ggactcgttc caagcctgtg ctcacaggga cacaccctgt gaacacaacg 120
 gtggacttcg gtgggacaac gtccttccag tgcaagggtg gcagtgacgt gaagcctgtg 180
 atccagtggc tgaagcgggt ggagtacggc tccgaggggac gccacaactc caccattgat 240
 gtgggtggcc agaagtttgt ggtgttgccc acgggtgatg tgtggtcacg gcctgatggc 300

tcttacctca acaagctgct catctctcgg gccccgccagg atgatgctgg catgtacatc 360
 tgcctagggtg caaataccat gggctacagt ttccgtagcg ccttcctcac tgtattacca 420
 g 421

<210> 141
 <211> 140
 <212> PRT
 <213> Mouse

<400> 141
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Glu Arg Thr Arg Ser Lys Pro Val Leu Thr
 20 25 30
 Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser
 35 40 45
 Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu
 50 55 60
 Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp
 65 70 75 80
 Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser
 85 90 95
 Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg
 100 105 110
 Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
 115 120 125
 Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 130 135 140

<210> 142
 <211> 67
 <212> DNA
 <213> Mouse

<400> 142
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgag 67

<210> 143
 <211> 22
 <212> PRT
 <213> Mouse

<400> 143
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg
 20

<210> 144
 <211> 1389
 <212> DNA
 <213> Mouse

<400> 144
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgaggac cccaagaat ggcagacaaa gtgggtcccac ggcaggtggc ccgcctgggc 120

cgactgtgc	ggctacagt	cccagtgag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggtg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatgtgga	tgaaggatga	ccagaccttg	360
acgcatctag	aggctagtga	acacagaaa	aagaagtgga	cactgagctt	gaagaacctg	420
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	480
gccacctaca	aagtggatgt	aatccagcgg	actcgttcca	agcctgtgct	cacagggaca	540
caccctgtga	acacaacggc	ggacttcggt	gggacaacgt	ccttccagt	caaggtgcgc	600
agtgacgtga	agcctgtgat	ccagtggtg	aagcgggtgg	agtacggctc	cgagggacgc	660
cacaactcca	ccattgatgt	gggtggccag	aagtttgtgg	tgttgcccac	gggtgatgtg	720
tggtcacggc	ctgatggctc	ctacctcaac	aagctgctca	tctctcgggc	ccgccaggat	780
gatgctggca	tgtacacctg	cctaggtgca	aataccatgg	gctacagttt	ccgtagcgcc	840
ttcctcactg	tattaccaga	ccccaaacct	ccagggcctc	ctatggcttc	ttcatcgtca	900
tccacaagcc	tgccatggcc	tgtggtgatc	ggcatcccag	ctggtgctgt	cttcaccta	960
ggcactgtgc	tgctctggct	ttgccagacc	aagaagaagc	catgtgcccc	agcatctaca	1020
cttcctgtgc	ctgggcatcg	tccccagg	acatcccag	aacgcagtgg	tgacaaggac	1080
ctgcccctcat	tggctgtggg	catatgtgag	gagcatggat	ccgccatggc	ccccagcac	1140
atcctggcct	ctgggtcaac	tgctggcccc	aagctgtacc	ccaagctata	cacagatgtg	1200
cacacacaca	cacatacaca	cacctgcact	cacacgctct	catgtggagg	gcaaggttca	1260
tcaacaccag	catgtccact	atcagtgcta	aatacagcga	atctccaagc	actgtgtcct	1320
gaggtaggca	tatgggggcc	aaggcaacag	gttggggagaa	ttgagaacaa	tggaggaaga	1380
gtatccttag						1389

<210> 145

<211> 462

<212> PRT

<213> Mouse

<400> 145

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10						15	
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20				25						30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
		35					40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65				70					75					80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
			85					90						95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Met
		100						105					110		
Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His
		115					120					125			
Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp
	130					135					140				
Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn
145					150				155					160	
Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val
			165					170					175		
Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr
			180					185					190		
Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln
	195					200					205				
Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr
	210					215					220				

Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val
225					230					235					240
Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg
				245					250					255	
Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr
			260					265					270		
Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro
		275					280					285			
Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu
	290					295					300				
Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu
305					310					315					320
Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala
				325					330					335	
Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser
			340					345					350		
Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile
		355					360					365			
Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser
	370					375					380				
Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val
385					390					395					400
His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly
				405					410					415	
Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr
			420					425					430		
Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg
		435					440					445			
Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser		
	450					455					460				